

Figure 1A

1	ACAAATGACCGGGAGCCATGACGTCATCGGGGGCGCAGGAAAGCAGGTGCTCTGCTGCTT	60
1	M T G S H D V I G G A G K Q V L C C F	19
61	TTGCAAGCAGAGAAATAAGAGTTTGGGCACCTACCCAGGGGTCCCAGGGAATGCCCTGTG	120
20	C K Q R N K S L <u>G T Y P G V P G N A L W</u>	39
121	GCTCCTGACCTCCCCCGCTGTAATGCTCTGAGCACTTCAGCAGTAATGCATGGAAGAGA	180
40	<u>L L T S P A C N A L S T S A</u> V M H G R D	59
181	TAAGGGGTCTGTGACCCATGGAAGTGTCCAAGTCCTCTCTGACACCCGCTTCTTTTCCTG	240
60	K G S V T H G T V Q V L S D T R F F S C	79
241	CCGTGAAGGACTACTTCCAGCAACCCAGTCTCCTGCCATGTCCGACCCCATCACGCTGAA	300
80	R E G L L P A T Q S P A M S <u>D P I T L N</u>	99
301	CGTCGGGGGAAGCTCTATACAACCTCACTGGCGACCCTGACCAGCTTCCCTGACTCCAT	360
100	<u>V G G K L Y T T S L A T L T S F P D S M</u>	119
361	GCTAGGCGCCATGTTTCAGCGGGAAGATGCCCACCAAGAGGGACAGCCAGGGCAACTGCTT	420
120	<u>L G A M F S G K M P T K R D S Q G N C F</u>	139
421	CATTGACCGTGACGGCAAAGTGTTCCGCTATATCCTCAACTTCCTGCGGACCTCCCACCT	480
140	<u>I D R D G K V F R Y I L N F L R T S H L</u>	159
481	TGACCTGCCTGAGGACTTCCAGGAGATGGGGCTGCTCCGCAGGGAGGCCGACTTCTACCA	540
160	<u>D L P E D F Q E M G L L R R E A D F Y Q</u>	179
541	GGTGCAGCCCCTGATTGAGGCCCTGCAGGAGAAGGAAGTGGAGCTCTCCAAGGCCGAGAA	600
180	<u>V Q P L I E A L Q E K E V</u> E L S K A E K	199
601	GAATGCCATGCTCAACATCACACTGAACCAGCGTGTGCAGACGGTCCACTTCACTGTGCG	660
200	N A M L N I T L N Q R V Q T V H F T V R	219
661	CGAGGCACCCCAGATCTACAGCCTCTCCTCTTCCAGCATGGAGGTCTTCAACGCCAACAT	720
220	E A P Q I Y S L S S S S M E <u>V F N A N I</u>	239
721	CTTCAGCACCTCCTGCCTCTTCTCAAGCTCCTTGGCTCTAAGCTCTTCTACTGCTCCAA	780
240	<u>F S T S C L F L K L L G S K L F Y C S</u> N	259
781	TGGCAATCTCTCCTCCATCACCAGCCACTTGCAGGACCCCAACCACCTGACTCTGGACTG	840
260	G N L S S I T S H L Q D P N H L T L D W	279
841	GGTGGCCAATGTGGAGGGCCTGCCAGAGGAGGAGTACACCAAGCAGAACCTCAAGAGGCT	900
280	V A N V E G L P E E E Y T K Q N L K R L	299

Figure 1B

901 CTGGGTGGTCCCCGCCAACAAAGCAGATCAACAGCTTCCAGGTCTTCGTGGAAGAGGTACT 960  
300 W V V P A N K Q I N S F Q V F V E E V L 319

961 GAAATCGCTCTGAGCGATGGCTTCTGCATCGATTCTTCTACCCACATGCTCTGGATTT 1020  
320 K I A L S D G F C I D S S H P H A L D F 339

1021 TATGAACAATAAGATTATTCGATTAATACGGTACAGGTAAAAGGACCCCAACAACACTGG 1080  
340 M N N K I I R L I R Y R 351

1081 AGATGGGGAGTCCCAGGAAGCTCATGTCAGCCAGGTCTTGGAGGGCATCTCGCCAGTGGT 1140

1141 GCGAGGCAGGGGACTATACTAATCTGTATTAATTGTGTAGCAGGACTTGATTCCCCCAT 1200

1201 GATGAAGTCCACCTTTTGGAAATCCAGTGTCTCTGAACAGAACACCTTTTTTCTTGCCA 1260

1261 TTTTGAGCTGCAGACAGGCGGTTTATTATGACAAGTGAAGAGTCAGCTGATGTGTACTAA 1320

1321 AGGAGGCCATAGGAGGATTTTCCAGCCAGGACAAAAGAGCAGCAGTTTTCTCCTGGGCTC 1380

1381 CATCTCTCTGTACCGCTAGCCAGTGCCGCATTTATCCATCTGTAAGAAGGCCCTGGTGA 1440

1441 GAGGATGGGATGAGAACAAGAGGCTACCTCCAGTTAACCAGGACATAAAGTCCCCAGCGG 1500

1501 TTCCTGTCACACCTGCTCCTCCCTCCCCAGGGTGCATCCATGATCGTGGATGTTTGCCCA 1560

1561 GGGGTGACCATGTTTGGCTGGCTTGAATGCTGTGCATTCTCAGAGCTCTGTTAGTGTCC 1620

1621 CCTCTTGGGGGTCAGAGATGAGGTGTGGCAGGGTCTAGAGGAATGAGTGTCCAGGCAGAG 1680

1681 TTCAGAAGGTAGGAATGTCCCTCTTGATAGGGCTGAATCAAGGGATTCTTGCTTTAGAA 1740

1741 AGGGTCTGCTATCTTTGCAAAAATGTGCAAGTATCTGTAGCCAGTGTAATGAAATCACTT 1800

1801 CCAAATCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1839

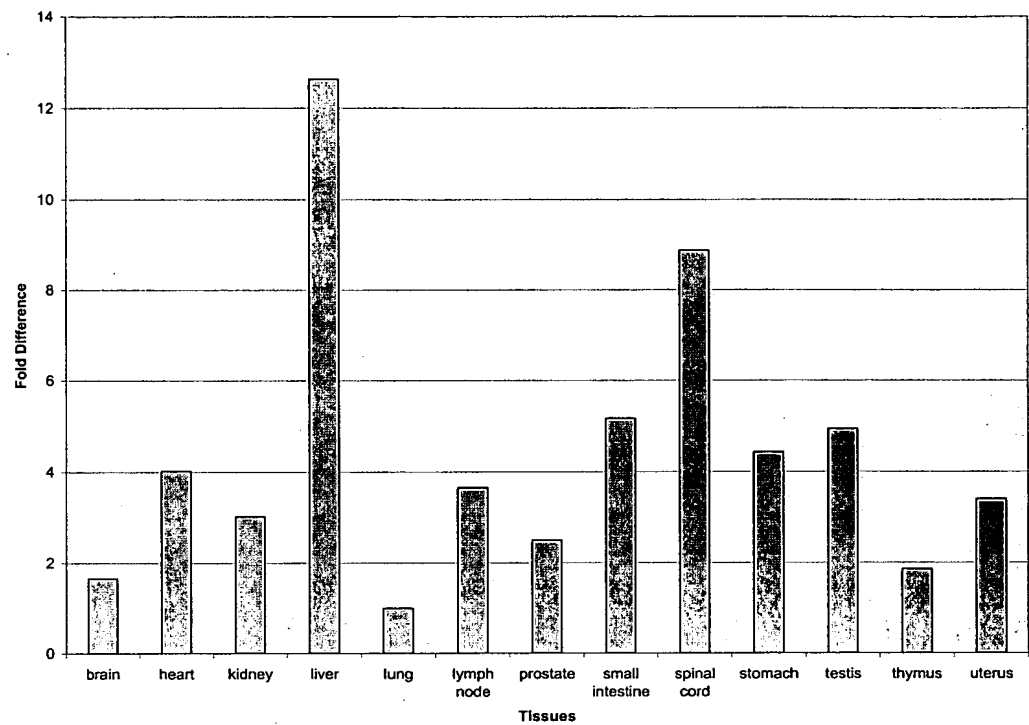
Figure 2A

		1		50
K+betaM4	(1)	-----	MTGSHDIVIGGAGKQVLCCFCKQRNKS LGTYPGVPGNALWLLT	
KCNMB1	(1)	-----		
K+Hnov28	(1)	-----		
K+Hnov27	(1)	-----		
CG10440	(1)	MDRERERDVKALEPRDLSSTGRIYARSDIKISSSPTVSPTISNSSSPTPT		
gi.12654691	(1)	-----		
		51		100
K+betaM4	(43)	SPACNALSTSAVMHGRDKGSVTHG----	TVOVLS DTRFFSCREGLPATO	
KCNMB1	(1)	-----	MVKKL VMAQKRCEPRALC	
K+Hnov28	(1)	-----	MDNGDW	
K+Hnov27	(1)	-----	MSRPLITRSPASPLXNOGIFTPAQ	
CG10440	(51)	PFASSSVTPLGLPGAVAAAAA VCGASSAGASSYLHGNHKPITGIPCVA		
gi.12654691	(1)	MPHRKERPSGSSLHTHGSTGTAE GGNMSRLSLITRSPVSPLAACGIFLP		
		101		150
K+betaM4	(89)	SEAMSDPITLNVGCKLYTISLATLTSEPD SMLGAMFSGKMP TKRDSQ-GN		
KCNMB1	(19)	LGVTMVCAVITYYILVTIVLPYQKSVWTOESKCELIETNIRDOELKG		
K+Hnov28	(7)	GYMMDPVTLNVGGHLYTISLATLTTRYPD SMLGAMFGGDFPTARDEQ-GN		
K+Hnov27	(25)	LTKSNAPVHIDVGGHMYTSSLATLT KYPESRTIGRLFDGTEPIVLD SLKQH		
CG10440	(101)	ASRYTAPVHIDVGGTITYTSSLETLT KYPESKLAKLFNGQIPIVLD SLKQH		
gi.12654691	(51)	LTKSNAPVHIDVGSIMYTSSLATLT KYPDSRTISRLFNGTEPIVLD SLKQH		
		151		200
K+betaM4	(138)	CFIDRDGKMFYRI LNFRLTSELDLPEDFOEMGLLRREADFYQOPIL EAL		
KCNMB1	(69)	KKVPQYPCLVNVSAAGRWAVLYHTEDTRDQ NQQCSYIPGSVDNYQTARA		
K+Hnov28	(56)	YFIDRDGPIFRYVLNFLRTSELTLPLDFKEFDLLRKEADFYQDEPIIQCL		
K+Hnov27	(75)	YFIDRDGOMFRYVLNFLRTSKLLLPDDFKDYTLLEYEAKYFOLQPMLE		
CG10440	(151)	YFIDRDGGMFRHILNFMNRSLILAE DFPDLELLLEEARYVEVPMIKOL		
gi.12654691	(101)	YFIDRDGETFRYVLSFLRTSKLLLPDDFKDFSLLYEEARYYQOLQPMVREL		
		201		250
K+betaM4	(188)	QEKVVELSKAEKNAMLNITLNQ RVQTVHFTVREAPQIYS--LSSSSMEV		
KCNMB1	(119)	DVEKVRKAFQ-----	EQQVFCFS--APRGNETS	
K+Hnov28	(106)	NDPKPLYPMD-----	TFEVVELS--STRKLSKY	
K+Hnov27	(125)	BRWKQDRETG-----	RFSRECEC--LWVRNAPDL	
CG10440	(201)	BSMRKQVRVNGNYLVAPPTPPARHIKTS PRTSASPECNYEVVALHISPD		
gi.12654691	(151)	BRWQOEQEQR-----	RRSRACDC--LWVRVTPDL	
		251		300
K+betaM4	(235)	FNANIESTSCLFLKLLGSKLFYCSN CNLSSITSHLODPNHITLDWMANVE		
KCNMB1	(146)	VLFORLYCPQALLFSLFWPTFLLTGGLLI IAMVKSNOYLSITMAAQ----		
K+Hnov28	(133)	SNPVAVIITQLTITTKVHSLLEGISNYFT KWNKAMMDTRCQVSFTFCPC		
K+Hnov27	(152)	GERITLSCDKSLIEEVFPETGDMCNSVN -AGWNH-DSTHVIREFPLNGYC		
CG10440	(251)	GERITLSAFRALDELFP EASOATQSSRS GVSWNQGDWQOTIRFPLNGYC		
gi.12654691	(178)	GERIALSGEKALIEEVFPETGDMCNSVN -AGWNQ-DPTHVIRFPLNGYC		
		301		350
K+betaM4	(285)	GLPEEEYTKQN LKRLWVPANKQIN-SFOVEVEEVLKIAISDGFCIDSSH		
KCNMB1	(192)	-----		
K+Hnov28	(183)	DYHQEVS LRVHMEYITKQCF TIRNTRVHHMSEANENTVEHNWTFCRLA		
K+Hnov27	(200)	HLNSVQVLERLQQRGFETIVSCGGGV DSSQFSEYVLRRERTRTPRVPSVI		
CG10440	(301)	KLNSVQV LTRLNAGETIEASVGG----	QQFSEYLLARRVPM-----	
gi.12654691	(226)	RLNSVQDVL-----		

## Figure 2B

		351		368
K+betaM4	(334)	PHAL	FMNNKIIRLIRYR	
KCNMB1	(192)	-----		
K+Hnov28	(233)	RKTD	-----	
K+Hnov27	(250)	RIKOEPL	-----	
CG10440	(339)	-----		
gi.12654691	(235)	-----		

Figure 3



**Figure 4.****K+betaM4**

<b>Protein</b>	<b>Genbank ID</b>	<b>Identities</b>	<b>Similarities</b>
human potassium channel K+Hnov27 protein	gi  Y34125	31.6%	45.1%
human potassium channel K+Hnov28 protein	gi  Y34129	42.3%	50.5%
human neuroblastoma protein	gi 12654691	36.2%	47.3%
Drosophila CG10440 protein	gi 7291303	28.0%	38.6%
Human Maxi-K potassium channel beta subunit, KCNMB1	gi 4758625	26.1%	39.1%

**K+betaM5**

<b>Protein</b>	<b>Genbank ID</b>	<b>Identities</b>	<b>Similarities</b>
human potassium channel K+Hnov28 protein	gi  Y34129	31.7%	43.4%
the human lung protein, MGC:2376	gi 12654469	34.4%	45.6%
human MSTP028 protein	gi 11640564	31.7%	43.4%
Caenorhabditis K+ channel tetramerisation domain containing protein	gi 3875362	34.4%	45.6%
Drosophila CG10465 protein	gi 7302243	30.8%	38.3%
Human Maxi-K potassium channel beta subunit, KCNMB1	gi 4758625	20.0%	40.0%

### Figure 5

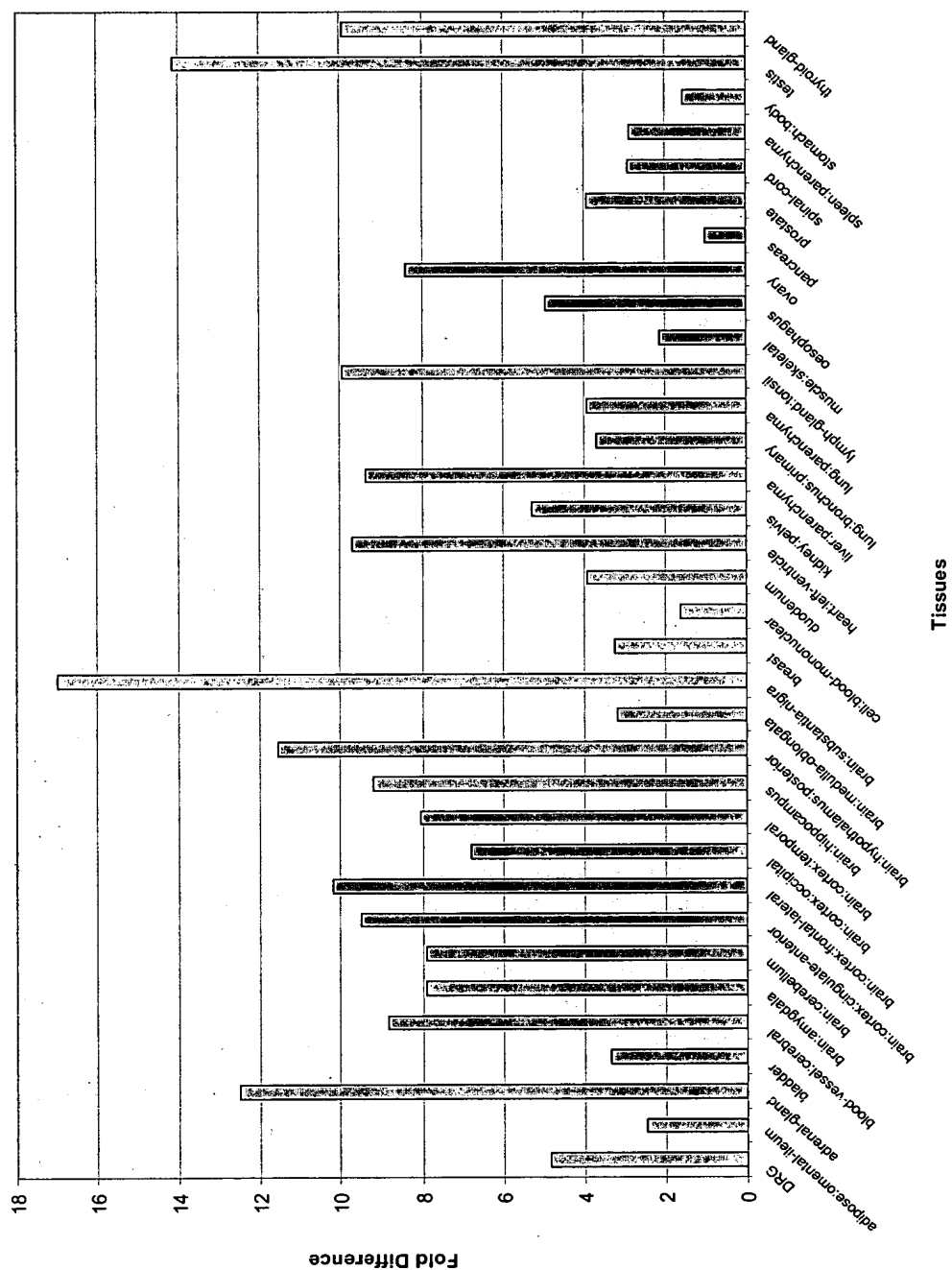


Figure 6A

```

1  ATGACGATGGCGGTTTTGCGGAATAGAAAAGGGGAAAGGGGACCACTCAGGCGCCGGCCG  60
1  M T M A V L R N R K G G K G P L R R R P  20

61  CTGGCGCTGCCTGCTCTTCGACTGGGCGAGCTTCCTGCCAATCAGGGCGGAACCAGCGCG  120
21  L A L P A L R L G E L P A N Q G G T S A  40

121  GCGTCGGCCAGTAGCGGGAGGCGGTCTGGGTCAGGCCCCAGCTGGGCGCGAGCGGGTCTGGC  180
41  A S A S S G R R S G Q A P A G R E R V G  60

181  GTTGAGGGAGCCACCGCCCTCCCGCCTGCGCACTGCCTCTCGCCCCCTCCGGCCAGCCC  240
61  V E G A T A L P P A H C L S P P S G Q P  80

241  GCAGCCGGCCGCGTCATGCCAGGCGCTGCTCGGCGAGCCAGAGGGATGGTGGTAGTCACG  300
81  A A G R V M P G A A R R A R G M V V V T  100

301  GGGCGGGAGCCAGACAGCCGTCGTCAGGACGGTGCCATGTCCAGCTCTGACCCGAAGAC  360
101  G R E P D S R R Q D G A M S S S D A E D  120

361  GACTTTCTGGAGCCGGCCACGCCGACGGCCACGCAGGCGGGGCACGCGCTGCCCTGCTG  420
121  D F L E P A T P T A T Q A G H A L P L L  140

421  CCACAGGAGTTTCCTGAGGTTGTTCCCTTAACATCGGAGGGGCTCACTTCACTACACGC  480
141  P Q E F P E V V P L N I G G A H F T T R  160

481  CTGTCCACACTGCGGTGCTACGAAGACACCATGTTGGCAGCCATGTTTCAGTGGGCGGCAC  540
161  L S T L R C Y E D T M L A A M F S G R H  180

541  TACATCCCCACAGACTCCGAGGGCCGGTACTTCATCGACCGAGATGGCACACACTTTGGA  600
181  Y I P T D S E G R Y F I D R D G T H F G  200

601  GATGTGCTGAATTTCTGCGCTCAGGGGACCTCCACCCAGGGAGCGTGTTTCGAGCTGTG  660
201  D V L N F L R S G D L P P R E R V R A V  220

661  TACAAAGAGGCCCCAGTACTATGCCATCGGGCCCCTCCTGGAGCAGCTGGAGAACATGCAG  720
221  Y K E A Q Y Y A I G P L L E Q L E N M Q  240

721  CCACTGAAGGGCGAGAAGGTGCGCCAAGCGTTTCTGGGACTCATGCCCTATTACAAAGAC  780
241  P L K G E K V R Q A F L G L M P Y Y K D  260

781  CACTTGGAGCGGATTGTGGAGATCGCCCGGCTGCGTGCGGTCCAGCGGAAGGCCGCTTT  840
261  H L E R I V E I A R L R A V Q R K A R F  280

```



Figure 6B

841	GCCAAGCTCAAGAGCTTGACACCTTCCTGGCTAATGAGTGTCTCATCAAGATGCCCCCT	900
281	<u>A K L K S L T P S W L M S V L I K M P P</u>	300
901	GGAGTCACATCATGGATTAAACGCAGAAAGGCGGCTGTATTTGGAAACTCCCATTGGTCCA	960
301	<u>G V T S W</u> I N A E R R L Y L E T P I G P	320
961	GAGAGACAGAACAAATGAGAAGAAATCCCCTGTCCAGTTGCCTGCAGGAGTATTCCAACAC	1020
321	E R Q N N E K K S P V Q L P A G V F Q H	340
1021	TTCATGGGCTAGAGGATTCCATTGAGATGGGGTTTACGTCTTGATTTTGAACACCTGTCA	1080
341	F M G	343
1081	GCACTGTTCTCTGTTTGCATGGCAATTCTGACCCTTTTATGGCAACAACACCCCTGGGAC	1140
1141	AACCCAGATTTGTAGATTGAGATCCAAAGGTAGAATTTCCAGACAGTCCAACCAAGGTAT	1200
1201	CAAGTGATGTTTCCAGAGTGGAAGGCTCTCACCGTGTCCAGGATTTCTGGGGTTTGTAA	1260
1261	GCAGTACTGGCCATTTGTGACCCTGTTTTTACCTAATCATTCTGTCTTTTTAGGACATG	1320
1321	GTTTTACCCGATCCCTGGCAAAGGATCCAGAATTCGAATAGCTGAAAACCCTGTTATAGC	1380
1381	TTTTCTCCTATTCTGCCTTACCCAAGACACACTTGAACCCCTCAGTAAGGCTATAGAGAG	1440
1441	GGCCATGAGCAGGGGCAGCCTCTCCCTTGTTTCTACAGCTCCATGATGAGGGGTTGACTG	1500
1501	AGGCCAGCAATCCTTGTTAGGTGTGACAGTTGCAATATAATTAACAGTTTCAAGATCTAGA	1560
1561	GGTACCTTTTGAAGAACCCTTCAGGGATATCTATCCACAGTAGCCTGGAGCAGCCAAG	1620
1621	GTGAACCTGAGATTTTGACCCACACAATAAGGGGGGGCCATTCTTTTTCAAATATTTTGG	1680
1681	CTTCAGAATACTTCATTACACATGCAAATATTGAGAGATTAACAGAAATTCCAGCTCT	1740
1741	TATGCCTAACTGAGAAGAGCCACTGCAAGTTGCAGTTAGGTACCCATGTGCAGCAGAGGC	1800
1801	CAGCTGAATCCCAGAGCTTCCCAAAGTGACACCAGCGGGGACTATTCTTGATGTCCCAC	1860
1861	CCAAGAGAGGAAGATGAGCTGAGGCGCTCTTGCTCTGCCCAAATGCATCCCATGTGCATT	1920

**Figure 6C**

1921 CACGTGTCACCCATTCAAAATAACATGGCATTCTTGGAACCTTGTATCTGACATGTAAGA 1980  
1981 CCAGCCTACACATTGGGGTGGGTGCAGGGGCTCACACTTGTAATCCTAGCACTTTGGAAG 2040  
2041 GCTGAGGTGGGCAGATTGCTTGAGCACAGGAGTTCCAGACCAGCCTGAGCAACATGGCGA 2100  
2101 AATCCTGTCTCTTCAAGAAATAAAATAATAATAATAAAAAAAAAAAAAAAAAA 2154

---

Figure 7A

		1	50
K+betaM5	(1)	MTMAVLNRNRKGGKGPLRRRPLALPALRLGELPANQGGTSAASASSGRRSG	
KCNMB1	(1)	-----	
CG10465	(1)	-----	
gi.12654469	(1)	-----	
K+Hnov28	(1)	-----	
MSTP028	(1)	-----	
K+channel_tetra	(1)	-----	
		51	100
K+betaM5	(51)	QAPAGRERVGVEGATALPPAHCLSPPSGQPAAGRVMPGAARRARGMVVVV	
KCNMB1	(1)	-----	
CG10465	(1)	-----	
gi.12654469	(1)	-----	
K+Hnov28	(1)	-----	
MSTP028	(1)	-----	
K+channel_tetra	(1)	-----	
		101	150
K+betaM5	(101)	GREPDSRRQDGAMSSSDAEDDFLEPATPTATQAGHALPLLQEFEEVPL	
KCNMB1	(1)	-----MVKKLVMA	
CG10465	(1)	-----MSEMSG-----DHKILLKGHS--SQYLLKL	
gi.12654469	(1)	-----MSTVEL	
K+Hnov28	(1)	-----MDNGDWGYMMDDPVTIL	
MSTP028	(1)	-----MEEMSGESVSSAVPAAATRSTTSFKGTSPSSKYVKL	
K+channel_tetra	(1)	-----MEPSTTVKL	
		151	200
K+betaM5	(151)	NVGGCHLYTTIRLSTLLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFG	
KCNMB1	(9)	QKRCESTRALCLGVMTMVCAVITYYLLVTTVLPLYQKSVWTOESKCHLIET	
CG10465	(24)	NVGGCHLYTTIRLSTLLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFG	
gi.12654469	(8)	NVGGCHLYTTIRLSTLLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFG	
K+Hnov28	(17)	NVGGCHLYTTIRLSTLLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFG	
MSTP028	(37)	NVGGCHLYTTIRLSTLLRCYEDTMLAAMFSGRHYIPTDSEGRYFIDRDGTHFG	
K+channel_tetra	(10)	DVGCKKTKTTTFTLCK-HDSMLKTMFCTDVPTKNEEGSVFIDRDGTHFG	
		201	250
K+betaM5	(201)	DVLNLSLRSCDLEPP--REK--VRVYKEAQYVAICPLLEQLENMQPLKGEK-	
KCNMB1	(59)	NIRDOELKGGKVPQYPCLVNVSAAGRNAVYHTESTRQONQCSYIPG	
CG10465	(74)	IILNMLRDGTPLPETNKEAEALLAEAKYVCTELAISCEALYAHQEPK	
gi.12654469	(58)	PILDYLRITGQVPT---QHTEVYREAOYVEIKPLVKKLLEDMPQIFGEQV	
K+Hnov28	(67)	YVLNLSLRITSEMLPLDFKEDLLRKEADEVOEPLIQCLNDPKPLYPMD-	
MSTP028	(86)	TILNMLRDGAVPLPESRETEELLAEAKYVLYOGLVEECQAAALQNKDYTE	
K+channel_tetra	(59)	LILNLSLRDQIALPDSDREVRVLAEEASYSLMDPLLELCGERLEQSLNP-	
		251	300
K+betaM5	(247)	-----VRQAFILG---LMPYYKDHLEKVEIAR-----LRVQR	
KCNMB1	(109)	SVDNMQARADVEKVRKFOEQQVFYCESAPR-----	
CG10465	(124)	PICRPLPITSQKEEQLLSVSLKPAVILVQRQNNKYSYTSSTDDNMLKN	
gi.12654469	(104)	SRKQPLQVPGYSENLEMMVRLARAEATTARK-----SSVVC	
K+Hnov28	(116)	---TEEVVELSSTRKLSKYSNPVAVITITQL-----TITTKVHSL	
MSTP028	(136)	PFCKVPVITSSKEEQKLITATSNKPAVKLLYNRSNNKYSYTSNSDDNMLKN	
K+channel_tetra	(108)	---YVHLVSTVLEARKLITFATEKPIVVLRLP-----VYIATSGNQSYIFS	
		301	350
K+betaM5	(277)	KARFAKLSLTPSWLMSVLIKMP-----GV--TSVINAERRLYLETPIGP	
KCNMB1	(141)	GNETSVLFQRLYGPAQLFSLFWP-----TELLTGGLLIHAMVKSNOY	
CG10465	(174)	TELFDKLSLRGNERITFKQVIGP---SEICQWSEYGHGKVAEVCCTSI	
gi.12654469	(142)	LVETEEQDAYVSEVLCFQDKKMFKSVVKFGPWKAVLDNSDLMHCLEMDI	
K+Hnov28	(153)	LEGTSNYFTKANKHMMDFRCQVS---FTFGPCDQHQEVSLRVHMEYIT	
MSTP028	(186)	TELFDKLSLRGNGRVLFTKQVIG---DEICQWSEYQGGRKTAECCTSI	
K+channel_tetra	(150)	ETKFRLESEEMHKHVAFTLITEPEF--NEDCSWSEFLRAKKTARIKG-P	

Figure 7B

		351		400
K+betaM5	(321)	ERQNNK	KSPVQLPAGVFQHF	MG-----
KCNMB1	(184)	SILAA	QK-----	
CG10465	(221)	VYATDR	KHKVEFPEAR	IYEETLQVLLYENRN--APDQELMQATSSARVG
gi.12654469	(192)	KAQGYKVFS	KFYLTYP	TKRNEFHFNISFTFTWW-----
K+Hnov28	(200)	KQGFTIR	NTRVHHMSE	RANENTVEHNWTFCLARKTDD-----
MSTP028	(232)	VYATEK	KQTKVEFPEAR	IYEETLNILLYEAQDGRGPDNALLEATG----
K+channel_tetra	(197)	MDCNLVE	ECMPKTVER	RREKKIWH-----
		401		440
K+betaM5	(344)	-----		
KCNMB1	(192)	-----		
CG10465	(269)	SASGTSINQYTSDEEEEERTGLARLSNKRNP	S-----	
gi.12654469	(226)	-----		
K+Hnov28	(238)	-----		
MSTP028	(277)	---	GAAGRSHHLDEDEERERI	ERVRRRIHIKRPDDRAHLHQ
K+channel_tetra	(221)	-----		

Figure 8

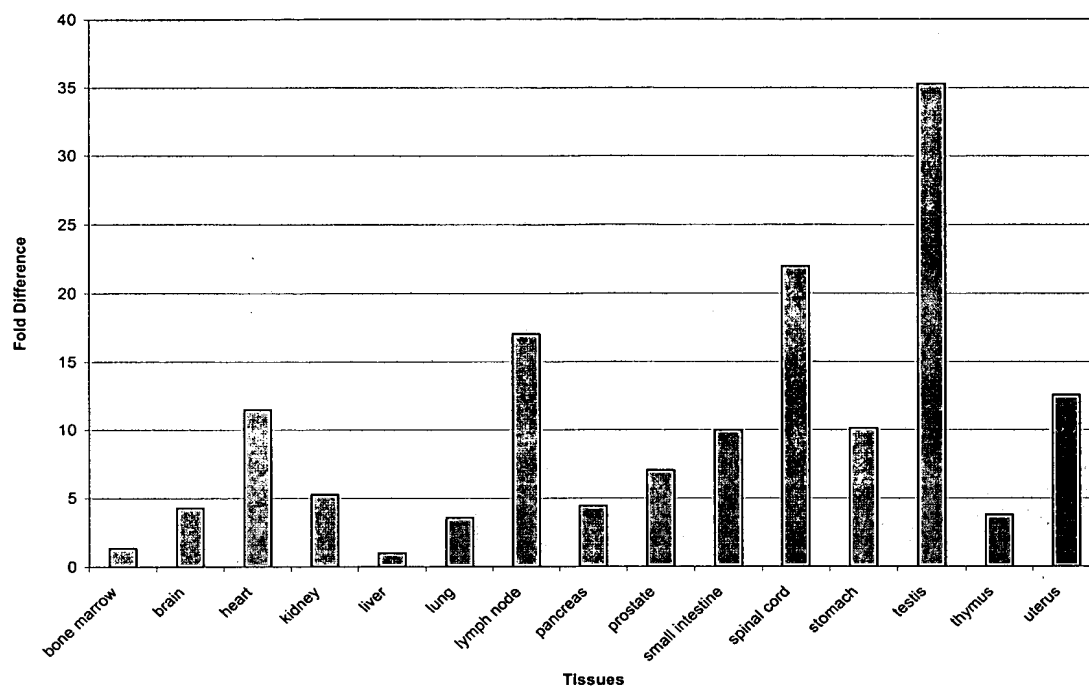


Figure 9

